Amendments to the Specification

Please replace the paragraph beginning at page 9, line 20 with the following amended paragraph:

The region r stretches from the beginning of, but not including the XPD gene, to approximately the end of ERCC1 and includes the genes RAI, LOC162978, and ASE-1. More specifically r is bounded by and includes the following two sequences: AGAACCCCCG CCCCTCCACC TCGTCTCAAA (bases 1 to 30 of SEQ ID NO:1) and TCCCTCCCCA GAGACTGCAC CAGCGCAGCC (bases 37761 to 37790 of SEQ ID NO:1), and is defined by SEQ ID NO: 1.

Please replace the paragraph beginning at page 9, line 29 with the following amended paragraph (note the "r" in the original text is shown here as r):

One preferred section of the region r stretches approximately from the end of RAI to the end of ASE-1 and includes the genes RAI, LOC162978, and ASE-1. More specifically, this section of r is bounded by and includes the following sequences: GAAGTGAGCC AAGATCACGC CACTGCACTC (bases 1522 to 1551 of SEQ ID NO:1) and GTGCCCACCT GGGCCACCAG AAGGTGACAC (bases 37723 to 37752 of SEQ ID NO:1). In the present context the region r means SEQ ID NO: 1 bases 1522-37752 and complementary sequence as well as transcriptional products and translational products thereof.

Please replace the paragraph beginning at page 10, line 1 with the following amended paragraph:

3

Finally, in the claims the gene RAI is defined as including transcribed sequences of the gene plus a 1500 base upstream promoter region. More specifically RAI is bounded by and includes the following sequences: CATAACCACA ATGATGAGCA TGTATTGAGT (bases 7761 to 7790 of SEQ ID NO:1) and ATGTTGTCCA GGCTGGTCTT GAACTCCTGA (bases 22856 to 22885 of SEQ ID NO:1). In the present context this section of the region relates to SEQ ID NO: 1 bases 7761-22885 and complementary sequence as well as transcriptional products and translational products thereof.

Please replace the paragraph beginning at page 13, line 6 with the following amended paragraph:

Table 1b

Identification in dbSNP[1]		Position in SEQ ID NO: 1
rs#3047560	ataaaaaaat aaaaaaaa (-/AA) atagccgagc atggtggtgg (SEQ ID NO:173)	4795-6
rs#5000150	tgttgtccaa gctggCAGAG (A/G) tttttgtttg tttgtttgag (bases 6888 to 6928 of SEQ ID NO:1)	6908
rs#4589665	CCAGGGCATA CAACCAGCAC (T/A) TGATTTTctg tgtgacctca (bases 20593 to 20633 of SEQ ID NO:1)	20613
rs#4803814	cctgcttgct tgctttctct (C/T) tctctctttc tttctttctt (bases 25630 to 25670 of SEQ ID NO:1)	25650
rs#4803815	cttgcttgct ttctctctct (C/T) tctttctttc tttctttctt (bases 25634 to 25674 of SEQ ID NO:1)	25654
rs#4572514	CTGTTCAGGC TGGCGGCTCA (C/T) TTGGATGAAC AGGGAGTGTG (bases 28671 to 28711 of SEQ ID NO:1)	28691
rs#4802252	agccaccaca cctggccAAA (C/T) CAGCTATTCT GAAAGGCCCC (bases 29666 to 29706 of SEQ ID NO:1)	29686
rs#4803816	GAGCCTATTG TTGGAAAGTT (C/T) TGAGTCCAAG ATTCTATCTT (bases 29795 to 29835 of SEQ ID NO:1)	29815
rs#4802253	CCTAACCCAG GGTTGCACTG (C/T) TCTGGAAGTC TAGATGGATG (bases 29902 to 29942 of SEQ ID NO:1)	29922
rs#4353560	GTAAGTGACt cttttttttt (C/T) ttttggtaga gatttagtct (bases 30419 to 30459 of SEQ ID NO:1)	30439
rs#3212989	TCGGGGACAG GACTG (C/T) GTCTTCTAGA GGCTCAGTGT (SEQ ID NO:174)	36994
rs#3212988	TGGCTGAGAC TCAAC (C/T) GTCACCCCCT CCTCTGGCTC (SEQ ID NO:175)	37068
rs#3212987	GTGTGACCTC TCTCT (-/TTC) TTCTTCTTCT TCTTCTTGGT (SEQ ID NO:176)	37431-37433
rs#3212986	GCTGCTGCTG CTGCT (T/G) CTTCCGCTTC TTGTCCCGGC (SEQ ID NO:177)	37660

Please replace the paragraphs beginning at page 13, line 28 with the following amended paragraphs:

Table 1c

Trivial name	Rs number	Sequence	Position
XRCC1e10	25487	GGCGGCTGCC CTCCC (A/G) GAGGTAAGGC CTCACACGCC (SEQ ID NO:178)	-
CKMe8	4884	AGTTGGAGAA AGGCCAGTCC AT (C/T) GACGACATGA (SEQ ID NO:179)	-
XPDe23	See ref 1	CGCTG (A/C) AGAGG (SEQ ID NO:180)	
XPDe10	See ref 1	TGCC (G/A) ACGAA (SEQ ID NO:181)	
XPDe6	See ref 1	TGCCG (C/A) TTCTA (SEQ ID NO:182)	
	3810366	CAATCCGCTA GGGCA (C/G) AGCCAATCGG GATACTGCGC (SEQ ID NO:183)	143 in SEQ NO 2
XPD_4bp	3916791	ttcgatcaat actca (-/GACA) atcttggcAG GCGCAGGAGG (SEQ ID NO:184)	323-326 in SEQ NO 2
XPDi4	1618536	tggctctgaa acttactagc cc (A/G) tatttatgg agagg (SEQ ID NO:185)	-
	3916790	caggcttgag ccacc (A/G) cgcccggccT GCAAAGCCAT (SEQ ID NO:186)	137 in SEQ NO 1
	3916789	gtagagacag gggtt (T/-) ctccatgttg gtcaggctgg (SEQ ID NO:187)	232 in SEQ NO 1
	3916788	ttagtagaga caggg (T/G) tttctccatg ttggtcaggc (SEQ ID NO:188)	235 in SEQ NO 1
	3916787	gctgcagtga gctgt (-/ACACCTGTGGTCCCAGCTACTCTGG AAGCTGAGGTGGGAGGATCGCTTGAGCCCAAGAGGTGGAGGCTGC AGTGAGCTGT) gactgtgcca ctgcactcca (SEQ ID NO:189)	632-633 in SEQ NO 1
XPD-5'2	2097215	TGACAGTAGA CATCCTGTCA T (A/G) ATAAGTCttt ttttttt (SEQ ID NO:190)	1610 in SEQ NO 1
RAI-3'	2377328	GGTTGAGAgg ccaggcg (C/T) ggtgctcacg cctgtaattt (SEQ ID NO:191)	7199 in SEQ NO 1
RAIe6	6966	ATTAAGTGCC TTCACACAGC (A/T) CTGGTTTAAT GTTTATAA (SEQ ID NO:192)	7887 in SEQ NO 1
RAIi5	4410192	CAGACCTCCC TCTCCCAATA (A/T) AACGGTTTGT CCTGTTGCC (SEQ ID NO:193)	10609 in SEQ NO 1
RAIi3	2017104	gggaggctcg aggcgggc (A/G) gattgcatga gctcaggatt (SEQ ID NO:194)	12190 in SEQ NO 1
RAIii1	1970764	tgcagtgagc tgagatcgc (A/G) ccactgcact ccagcctggg (SEQ ID NO:195)	15798 in SEQ NO 1
RAI-5UTR	4589665	CAGGGCATA CAACCAGCAC (A/T) TGATTTTctg tgtgacctca (SEQ ID NO:196)	-
RAI-5'2	4803814	cctgcttgct tgctttctct (C/T) tctctctttc tttctttc (SEQ ID NO:197)	25650 in SEQ NO 1
RAI-5'3	4803815	cttgcttgct ttctctctct (C/T) tctttctttc tttctttc (SEQ ID NO:198)	25564 in SEQ NO 1
RAI-5'	4572514	CTGTTCAGGC TGGCGGCTCA (C/T) TTGGATGAAC AGGGAGTG (SEQ ID NO:199)	28691 in SEQ NO 1
ASE1-5'2	2226949	TCTTAGGACG CATGGGGGT (G/T) GAGAGAACGG GGAGATAGA SEQ ID NO:200)	32035 in SEQ NO 1
	4803817	TCGGGGATTC GAACCCCTAT (r) CTACCCAAAG ACTCGGCTTC (SEQ ID NO:201)	32885 in SEQ NO 1
ASE1e1	967591	GCAGCCCGGG CTACAGGGTT (A/G) CCTGAGGTGT GGGTCCCAGG (SEQ ID NO:202)	34858 in SEQ NO 1
	5828233	aagactctct caaaaaaaaa (A/-) caaaaaaaaa acaaaaaaC CTTCCCTCTC CTGTTCCACT (SEQ ID NO:203)	36241 in SEQ NO 1
ASE1e3a	735482	AAGCCCAAAG GGA (A/C) AGAAACCTTC GAGCCAGAAG (SEQ ID NO:204)	36926 in SEQ NO 1
ERCC1-3'	762562	AGCCAGAAGG AGCG (A/G) AGCCTCAGGC CCAGGCAGCT (SEQ ID NO:205)	37267 in SEQ NO 1

ASE1e3b	2336219	AGAAAGAAAA ACAGCAA (A/G) ATGCCACAGT GGAGCCAGAG (SEQ ID NO:206)	-
ERCC1e4	See ref 1	GGCAC (G/A) TTGCG (SEQ ID NO:207)	
ERCC1e3	See ref 1	GGGCA (C/T) GTGGC (SEQ ID NO:208)	
FOSBe4	1049698	CACCCTTTTT TTGGGGTGCC (C/T) AGGTTGGTTT CCCCTGCA (SEQ ID NO:209)	-
SLC1A5e8	1060043	GCAGGACTCC TCCAAAATTA (C/T) GTGGACCGTA CGGAGTCG (SEQ ID NO:210)	-
LIG1e6	20580	AGAGGCTGAA GTGGC (A/C) ACAGAGAAGG AAGGAGAAGA (SEQ ID NO:211)	-
GLTSCR1e1	1035938	ccTGAGCAAA CCCATGAG (C/T) GTCCACCTCC TGAACCAAGG (SEQ ID NO:212)	-

Please replace the paragraphs beginning at page 15, line 1 with the following amended paragraphs:

rs#4589665	CCAGGGCATA CAACCAGCAC (T/A) TGATTTTctg tgtgacctca (bases 20593 to 20633 of SEQ ID NO:1)	20613
rs#4803814	cctgcttgct tgctttctct (C/T) tctctcttc tttctttctt (bases 25630 to 25670 of SEQ ID NO:1)	25650
rs#4803815	cttgcttgct ttctctctct (C/T) tctttcttc tttctttctt (bases 25634 to 25674 of SEQ ID NO:1)	25654
rs#4572514	CTGTTCAGGC TGGCGGCTCA (C/T) TTGGATGAAC AGGGAGTGTG (bases 28671 to 28711 of SEQ ID NO:1)	28691
rs#4802252	agccaccaca cctggccAAA (C/T) CAGCTATTCT GAAAGGCCCC (bases 29666 to 29706 of SEQ ID NO:1)	29686
rs#4803816	GAGCCTATTG TTGGAAAGTT (C/T) TGAGTCCAAG ATTCTATCTT (bases 29795 to 29835 of SEQ ID NO:1)	29815
rs#4802253	CCTAACCCAG GGTTGCACTG (C/T) TCTGGAAGTC TAGATGGATG (bases 29902 to 29942 of SEQ ID NO:1)	29922
rs#4353560	GTAAGTGACt cttttttttt (C/T) ttttggtaga gatttagtct (bases 30419 to 30459 of SEQ ID NO:1)	30439
rs#3212989	TCGGGGACAG GACTG (C/T) GTCTTCTAGA GGCTCAGTGT (SEQ ID NO:174)	36994

Please replace the paragraphs beginning at page 15, line 11 with the following amended paragraphs:

RAI-3'	2377328	GGTTGAGAgg ccaggcg (C/T) ggtgctcacg cctgtaattt (SEQ ID NO:191)	7199 in SEQ NO 1
RAIe6	6966	ATTAAGTGCC TTCACACAGC (A/T) CTGGTTTAAT GTTTATAA (SEQ ID NO:192)	7887 in SEQ NO 1
RAIi5	4410192	CAGACCTCCC TCTCCCAATA (A/T) AACGGTTTGT TCCTGTTGCC (SEQ ID NO:193)	10609 in SEQ NO 1
RAIi3	2017104	gggaggctcg aggcgggc (A/G) gattgcatga gctcaggatt (SEQ ID NO:194)	12190 in SEQ NO 1
RAIi1	1970764	tgcagtgagc tgagatcgc (A/G) ccactgcact ccagcctggg (SEQ ID NO:195)	15798 in SEQ NO 1
RAI-5UTR	4589665	CAGGGCATA CAACCAGCAC (A/T) TGATTTTctg tgtgacctca (SEQ ID NO:196)	-
RAI-5'2	4803814	cctgcttgct tgctttctct (C/T) tctctctttc tttctttc (SEQ ID NO:197)	25650 in SEQ NO 1
RAI-5'3	4803815	cttgcttgct ttctctctct (C/T) tctttcttc tttctttc (SEQ ID NO:198)	25564 in SEQ NO 1
RAI-5'	4572514	CTGTTCAGGC TGGCGGCTCA (C/T) TTGGATGAAC AGGGAGTG (SEQ ID NO:199)	28691 in SEQ NO 1
ASE1-5'2	2226949	TCTTAGGACG CATGGGGGT (G/T) GAGAGAACGG GGAGATAGA (SEQ ID NO:200)	32035 in SEQ NO 1

	4803817	TCGGGGATTC GAACCCCTAT (r) CTACCCAAAG ACTCGGCTTC (SEQ ID NO:201)	32885 in SEQ NO 1
ASE1e1	967591	GCAGCCCGGG CTACAGGGTT (A/G) CCTGAGGTGT GGGTCCCAGG (SEQ ID NO:202)	34858 in SEQ NO 1
	5828233	aagactctct caaaaaaaaa (A/-) caaaaaaaaa atcaaaaaaC CTTCCCTCTC CTGTTCCACT (SEQ ID NO:203)	36241 in SEQ NO 1
ASE1e3a	735482	AAGCCCAAAG GGA (A/C) AGAAACCTTC GAGCCAGAAG (SEQ ID NO:204)	36926 in SEQ NO 1

Please replace the paragraphs beginning at page 15, line 16 with the following amended paragraphs:

RAI-3'	2377328	GGTTGAGAgg ccaggcg (C/T) ggtgctcacg cctgtaattt (SEQ ID NO:191)	7199 in SEQ NO 1
RAIe6	6966	ATTAAGTGCC TTCACACAGC (A/T) CTGGTTTAAT GTTTATAA (SEQ ID NO:192)	7887 in SEQ NO 1
RAIi5	4410192	CAGACCTCCC TCTCCCAATA (A/T) AACGGTTTGT TCCTGTTGCC (SEQ ID NO:193)	10609 in SEQ NO 1
RAIi3	2017104	gggaggctcg aggcgggc (A/G) gattgcatga gctcaggatt (SEQ ID NO:194)	12190 in SEQ NO 1
RAIii1	1970764	tgcagtgagc tgagatcgc (A/G) ccactgcact ccagcctggg (SEQ ID NO:195)	15798 in SEQ NO 1
RAI-5UTR	4589665	CAGGGCATA CAACCAGCAC (A/T) TGATTTTctg tgtgacctca (SEQ ID NO:196)	-
RAI-5'2	4803814	cctgcttgct tgctttctct (C/T) tctctctttc tttctttc (SEQ ID NO:197)	25650 in SEQ NO 1
RAI-5'3	4803815	cttgcttgct ttctctctct (C/T) tctttctttc tttctttc (SEQ ID NO:198)	25564 in SEQ NO 1
RAI-5'	4572514	CTGTTCAGGC TGGCGGCTCA (C/T) TTGGATGAAC AGGGAGTG (SEQ ID NO:199)	28691 in SEQ NO 1

Please replace the paragraphs beginning at page 26, line 7 through page 27, line 28 with the following amended paragraphs:

1. GCTCTGAAAC TTACTAGCCC(A/G)GTATTTATGG AGAGGCATTT (SEQ ID NO:3)

2. GTGGTCAAAT TCTCATTCAT CGTGG (T/C) CCAGGCAAGC ACACTTCCTC (SEQ ID NO:4)

3. ACCCTGAGGT GAGCACCTGT TCCTT(C/T) TCCTTGCCCT TAGCCCAGAG GTAGA (SEQ ID NO:5)

4. GGGCAGGGGT TTGTGCCTCC AATGA (G/A) CACAAGCTCC CCCTGCCCCC CAACT (SEQ ID NO:6)

5. CCTGGCGGTG GCCGTCACCA GCTTT (T/C) GGGGGTGTTT GGGAAGCTGG (SEQ ID NO:75)

6. CTCCAGCCCC ACTGTTCCCT (A/G) GGCCCTATTG GTCCCCCTGG (SEQ ID NO:76)

7. ACAAGGAGGA GGCAGAAGTG AGGTT (G/C) AAACCCACTG CCCAATCTTA (SEQ ID NO:77)

8. CCAACACGGT GAAACCCCGT CTGTA(T/C)TAAAAATACA AAAATTAGCC (SEQ ID NO:78)

9. AATCCAGGAC CCCATAATCT TCCGT (C/T) ATCTAAAACA ATAATGGTGA (SEQ ID NO:79)

10. CCCAAGGGGG CGAGGGGAGG GTGAA (A/G)GGGTGGGACG GGGGCAGCCG (SEQ ID NO:80)

11. GAAGTGAGAA GGGGGCTGGG GGTCG (G/-) CGCTCGCTAG CGGGCGCGGG (SEQ ID NO:81)

12. CGCACGCGCA GTATCCCGAT TGGCT (C/G)TGCCCTAGCG GATTGACGGG (SEQ ID NO:82)

13. AACTCCTGGG TTCGATCAAT ACTCA (GACA/-) ATCTTGGCAG GCGCAGGAGG (SEQ ID NO:83)

14. GCTGGGATTA CAGGCTTGAG CCACC (A/G) CGCCCGGCCT GCAAAGCCAT (SEQ ID NO:84)

15. TTTTGTATCT TTAGTAGAGA CAGG (T/G) TTTCTCCATG TTGGTCAGGC (SEQ ID NO:85)

16. GCCTCAGCCT CCCGAGTAGC TGAGACT (C/A) CAGGTGCCCG CCACCACGCC (SEQ ID NO:86)

17. TGAAATTGTA GGTTGAGAGG CCAGGCG (C/T) GGTGCTCACG CCTGTAATTT (SEQ ID NO:87)

18. GTTTATAAAC ATTAAACCAG (T/A) GCTGTGTGAA GGCACTTAAT (SEQ ID NO:88)

19. CCGTCTCTAT TAAAAATATA AAA (A/C) AATTTAGCCG GGTGTAGCGG (SEQ ID NO:89)

20. GGGAGGCTCG AGGCGGGC (A/G) GATTGCATGA GCTCAGGATT (SEQ ID NO:90)

21. TCCCAAGTTT CAGGGCCCAA (T/G) ATTCTCAAAT CACAGGATTC (SEQ ID NO:91)

22. TGCAGTGAGC TGAGATCGC (A/G) CCACTGCACT CCAGCCTGGG (SEQ ID NO:92)

23. TCTTAGGACG CATGGGGGT (T/G) GAGAGAACGG GGAGATAGAC (SEQ ID NO:93)

24. CTGGGTTCTA GAACTACC (C/T) ATGCAAACCC AGCTGTTTCC (SEQ ID NO:94)

25. ATTCTGCCCT GGGTTCTAGA ACTACCT (C/A) TGCAAACCCA GCTGTTTCCC (SEQ ID NO:95)

8

26. GCTGTTTCCC ACCCCATAAG GCA (A/G) TAGGGGAGCC CACCTCCGCC (SEQ ID NO:96)

27. GACCTAGAAG ATCGGTCGAG A (C/T) AGCAGCTTGA GGCTGGCAGG (SEQ ID NO:97)

28. CTGGCCAGGA ATGCAGTCGG GTCAC (C/T) CTGTCTAGCC ACCGTCTCGC (SEQ ID NO:98)

29. GGGAGGAGTC GCCGATCAGG (C/T) CCCTTCCTGA AAGTCATCGA (SEQ ID NO:99)

30. GCAGCCCGGG CTACAGGGTT (A/G) CCTGAGGTGT GGGTCCCAGG (SEQ ID NO:100)

31. TAGAAATACT AACAAAGGGC (T/C) GTGGGTTTCT CCCCCTGCTT (SEQ ID NO:101)

32. ACAGGAGAGG GAAGGTTTTTTG (A/T) TTTTTTTTTT GTTTTTTTTT (SEQ ID NO:102)

33. GAAGAGGAAG AAGCCCAAAG GGA (A/C) AGAAACCTTC GAGCCAGAAG (SEQ ID NO:103)

34. GCGCCTCAAC AGCCAGAAGG AGCG (A/G) AGCCTCAGGC CCAGGCAGCT (SEQ ID NO:213)

35. TTGAGACTCT CTGTTTGAT (A/G) CTTCACTCAG AAGGTGCTTC (SEQ ID NO:105)

36. AGGCCAGGCT CCTGCTGGCT G (C/G) GCTGGTGCAG TCTCTGGGGA (SEQ ID NO:106)

37. CCCCTATACC CTCAAGCAT (C/T) TATCCATTGA GTTACAAACA (SEQ ID NO:107)

38. ACCATCCCCC GCCTTCCGTT (A/C) GTCCGGCCCC CGAGGCTAGC (SEQ ID NO:108)

Please replace the paragraphs beginning at page 27, line 33 through page 28, line 21 with the following amended paragraphs:

1. TGAAATTGTA GGTTGAGAGG CCAGGCG (C/T) GGTGCTCACG CCTGTAATTT (SEQ ID NO:87)

2. GTTTATAAAC ATTAAACCAG (T/A) GCTGTGTGAA GGCACTTAAT (SEQ ID NO:88)

3. CCGTCTCTAT TAAAAATATA AAA (A/C) AATTTAGCCG GGTGTAGCGG (SEQ ID NO:89)

4. GGGAGGCTCG AGGCGGGC (A/G) GATTGCATGA GCTCAGGATT (SEQ ID NO:90)

5. TCCCAAGTTT CAGGGCCCAA (T/G) ATTCTCAAAT CACAGGATTC (SEQ ID NO:91)

6. TGCAGTGAGC TGAGATCGC (A/G) CCACTGCACT CCAGCCTGGG (SEQ ID NO:92)

7. TCTTAGGACG CATGGGGGT (T/G) GAGAGAACGG GGAGATAGAC (SEQ ID NO:93)

8. CTGGGTTCTA GAACTACC (C/T) ATGCAAACCC AGCTGTTTCC (SEQ ID NO:94)

9. ATTCTGCCCT GGGTTCTAGA ACTACCT (C/A) TGCAAACCCA GCTGTTTCCC (SEQ ID NO:95)

10. GCTGTTTCCC ACCCCATAAG GCA (A/G) TAGGGGAGCC CACCTCCGCC (SEQ ID NO:96)

11. GACCTAGAAG ATCGGTCGAG A (C/T) AGCAGCTTGA GGCTGGCAGG (SEQ ID NO:97)

12. CTGGCCAGGA ATGCAGTCGG GTCAC (C/T) CTGTCTAGCC ACCGTCTCGC (SEQ ID NO:98)

13. GGGAGGAGTC GCCGATCAGG (C/T) CCCTTCCTGA AAGTCATCGA (SEQ ID NO:99)

14. GCAGCCCGGG CTACAGGGTT (A/G) CCTGAGGTGT GGGTCCCAGG (SEQ ID NO:100)

15. TAGAAATACT AACAAAGGGC (T/C) GTGGGTTTCT CCCCCTGCTT (SEQ ID NO:101)

16. ACAGGAGAGG GAAGGTTTTTG (A/T) TTTTTTTTT GTTTTTTTT (SEQ ID NO:102)

17. GAAGAGGAAG AAGCCCAAAG GGA (A/C) AGAAACCTTC GAGCCAGAAG (SEQ ID NO:103)

18. GCGCCTCAAC AGCCAGAAGG AGCG (A/G) AGCCTCAGGC CCAGGCAGCT
    (SEQ ID NO:213)

Please replace the paragraphs beginning at page 28, line 26 with the following amended paragraphs:

1. GTTTATAAAC ATTAAACCAG (T/A) GCTGTGTGAA GGCACTTAAT (SEQ ID NO:88)

2. CCGTCTCTAT TAAAAATATA AAA (A/C) AATTTAGCCG GGTGTAGCGG (SEQ ID NO:89)

3. GGGAGGCTCG AGGCGGGC (A/G) GATTGCATGA GCTCAGGATT (SEQ ID NO:90)

4. TCCCAAGTTT CAGGGCCCAA (T/G) ATTCTCAAAT CACAGGATTC (SEQ ID NO:91)

5. TGCAGTGAGC TGAGATCGC (A/G) CCACTGCACT CCAGCCTGGG (SEQ ID NO:92)

Please replace the paragraphs beginning at page 43, line 8 with the following amended paragraphs:

Table 7. Design of primers and fluorogenic probes for LightCycler

ASE1 e1

    Forward primer: 5'-GGTTTTCTGCTCTGCACACG <u>(SEQ ID NO:109)</u>

    Reverse primer: 5'-CCTTTCTCCTTCCACCAACG <u>(SEQ ID NO:110)</u>

    Anchor probe: 5'-TCTGCAACCTGGTGCGAGCAGC-Fluorescein <u>(SEQ ID NO:111)</u>

    Sensor probe: 5'-LCRed640-CGGGCTACAGGGTTACCTGAG-p <u>(SEQ ID NO:112)</u>

CKM e8

    Forward primer: 5'-TTGAAACTGGAACTCTGAGAAGG <u>(SEQ ID NO:113)</u>

    Reverse primer: 5'-TGGTGGATGGTGTGAAGCA <u>(SEQ ID NO:114)</u>

    Anchor probe: 5'-LC Red 640-CCTTTCTCCAACTTCTTCTCCATTTCCACC-p <u>(SEQ ID NO:115)</u>

    Sensor probe: 5'-GGGGATCATGTCGTCAATGGACT –Fluorescein <u>(SEQ ID NO:116)</u>

ERCC1 e4

    Forward primer: 5'-AGGACCACAGGACACGCAGA-3' <u>(SEQ ID NO:117)</u>

    Reverse primer: 5'-CATAGAACAGTCCAGAACAC-3' <u>(SEQ ID NO:118)</u>

    Anchor probe: 5'-LCRed640-TGGCGACGTAATTCCCGACTATGTGCTG p-3' <u>(SEQ ID NO:119)</u>

    Sensor probe: 5'-CGCAACGTGCCCTGGGAAT-Fluorescein <u>(SEQ ID NO:120)</u>

FOSB e4

    Forward primer: 5'-AGGCTCAACAAGGAAAAATGC <u>(SEQ ID NO:121)</u>

    Reverse primer: 5'-GCTAGACAGTCAAGGAGGGACG <u>(SEQ ID NO:122)</u>

    Anchor probe: 5'-LCRed 640-AAAGGGTGGGTGTGGGAGACATTGG-p <u>(SEQ ID NO:123)</u>

    Sensor probe: 5'-AAACCAACCTAGGCACCCAAA-Fluorescein <u>(SEQ ID NO:124)</u>

GLTSCR1 e1

    Forward primer: 5'-CGACGAACTTCTCTGAAGCGAA <u>(SEQ ID NO:125)</u>

    Reverse primer: 5'-AGCGACACGGGCATCTGG <u>(SEQ ID NO:126)</u>

    Anchor probe: 5'-ATGAGCGTCCACCTCCTGAACC-fluorescein <u>(SEQ ID NO:127)</u>

    Sensor probe: 5'-LCRed 640-AGGCAGCAGCATCGTCATCCCC-p <u>(SEQ ID NO:128)</u>

LIG1 e6

Forward primer: 5'-ATGCCCTGTAGGTTCAATGG (SEQ ID NO:129)

Reverse primer: 5'-TGGAGGTCTTTAGGGGCTTG (SEQ ID NO:130)

Anchor probe: 5'-GGCTGGTCCCGTCTTCTCCTTCC-Fluorescein (SEQ ID NO:131)

Sensor probe: 5'-LC Red 640-TCTCTGTTGCCACTTCAGCCTC-p (SEQ ID NO:132)

RAI i1

Forward primer: 5'-TGGCTAACACGGTGAAACC (SEQ ID NO:133)

Reverse primer: 5'-GGAATCCAAAGATTCTATGATGG (SEQ ID NO:134)

Anchor probe: 5'-GGGAGGCGGAGCTTGCAGTGA-Fluorescein (SEQ ID NO:135)

Sensor probe: 5'-LCRed 640-CTGAGATCGCACCACTGCAC-p (SEQ ID NO:136)

SLC1A5 e8

Forward primer: 5'-CAGTGTCCAAAGAGCACC (SEQ ID NO:137)

Reverse primer: 5'-CTACCCCTTTAGCGACC (SEQ ID NO:138)

Anchor probe: 5'-LCRed 640-TCCTGCCCCAGAGCGTCACC-p (SEQ ID NO:139)

Sensor probe: 5'-GTACGGTCCACATAATTTTGGAGGA-Fluorescein (SEQ ID NO:140)

XPD e10

    Forward primer: 5'-GATCAAAGAGACAGACGAGC <u>(SEQ ID
NO:141)</u>
    Reverse primer: 5'-GAAGCCCAGGAAATGC <u>(SEQ ID
NO:142)</u>
    Anchor probe: 5'-GGACGCCCACCTGGCCAACC-Fluorescein
<u>(SEQ ID NO:143)</u>
    Sensor probe: 5'-LCRed640-CGTGCTGCCCAACGAAGTG-p
(SEQ ID NO:144)

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    *Please replace the paragraphs beginning at page 45, line
1 with the following amended paragraphs:*

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Table 8. Primers and restriction enzymes used for typing of SNPs using PCR-RFLP

Gene exon		Primers	Enzyme	Digested Fragments
XRCC1 exon10		TTGTGCTTTCTCTGTGTCCA (SEQ ID NO:145)	MspI	240, 375bp (A)
		TATCAGAAAAGGCTGGAGGA (SEQ ID NO:146)		615bp (G)
ERCC1 exon4		AGGACCACAGGACACGCAGA (SEQ ID NO:147)	BsrDI	157, 368bp (A);
		CATAGAACAGTCCAGAACAC (SEQ ID NO:148)		525bp (G)
XPD exon6	1.set	CACACCTGGCTCATTTTTGTAT (SEQ ID NO:149)	*Tfi*I	
		TCATCCAGGTTGTAGATGCCA (SEQ ID NO:150)		
	2.set	TGGAGTGCTATGGCACGATCTCT (SEQ ID NO:151)	*Tfi*I	56, 114, 482 bp (A);
		CCATGGGCATCAAATTCCTGGGA (SEQ ID NO:152)		56, 596 bp (C)
XPD exon23	1.set	GTCCTGCCCTCAGCAAAGAGAA (SEQ ID NO:153)		
		TTCTCCTGCGATTAAAGGCTGT (SEQ ID NO:154)		
		ATCCTGTCCCTACTGGCCATTC (SEQ ID NO:155)	*Pst*I	66, 100, 158 (C);
		TGTGAACGTGACAGTGAGAAAT (SEQ ID NO:156)		100, 224 (A)

Please replace the paragraph beginning at page 45, with the following amended paragraph:

Table 9. Design of primers and SNaPshot primers for SNaPshot typing on sequenator.

XRCC1 exon7

Forward primer: 5'-GTCCCATAGATAGGAGTGAAAG (SEQ ID NO:157)

Reverse primer: 5'-CCCTAGGACACAGGAGCACA (SEQ ID NO:158)

SNaPshot primer: 5'-TGCATAGCTAGGTCCTGC (SEQ ID NO:159)

XRCC1 exon17

Forward primer: 5'-GCCAAGCAGAAGAGACAAA (SEQ ID NO:160)

Reverse primer: 5'-GAGTGGCTGGGGAGTAGGA (SEQ ID NO:161)

SNaPshot primer:

5'-AACTGACRAAACTAGCTCTATGGGGTGGTGCCGCA (SEQ ID NO:162)

RAI exon6

Forward primer: 5'-CCTACCACCATCATCACATCC (SEQ ID NO:163)

Reverse primer: 5'-GCCTTGCCAAAAATCATAACC (SEQ ID NO:164)

SNaPshot primer: 5'-CCTCTCCCCAATTAAGTGCCTTCACACAGC (SEQ ID NO:165)

XPD intron4

Forward primer: 5'-CGCAAAAACTTGTGTATTCACC (SEQ ID NO:166)

Reverse primer: 5'-CCCATTTTTATCATCAGCAACC (SEQ ID NO:167)

SNaPshot primer: 5'-CTGGCTCTGAAACTTACTAGCCC (SEQ ID NO:168)

Please delete the paragraphs at page 46, lines 1-6 (i.e., the entire table 10). Please insert the following new paragraph at page 46, line 1.

Table 10. Design of primers and probes for Taqman.

XRCC1 exon10

Forward primer: 5'-GCT GGA CTG TCA CCG CAT G (SEQ ID NO:169)

Reverse Primer: 5'-GGA GCA GGG TTG GCG TG (SEQ ID NO:170)

Probe (A): 5'Fam- TGC CCT CCC <u>A</u>GA GGT AAG GCC T –Tamra (SEQ ID NO:171)

Probe (G): 5'Vic - CCC TCC C<u>G</u>G AGG TAA GGC CTC –Tamra (SEQ ID NO:172)

Please replace the paragraph beginning at page 53, line 3 with the following amended paragraph:

The following depicts the region r stretching from the beginning of, but not including the XPD gene, to approximately the end of ERCC1, and includes the genes RAI, LOC162978, and ASE-1. More specifically r is bounded by and includes the following two sequences: AGAACCCCCG CCCCTCCACC TCGTCTCAAA (bases 1 to 30 of SEQ ID NO:1) and TCCCTCCCCA GAGACTGCAC CAGCGCAGCC (bases 37761 to 37790 of SEQ ID NO:1), and is defined by SEQ ID NO: 1.

Please replace the paragraph beginning at page 53, line 3 with the following amended paragraph:

The following depicts the region s as described above. More specifically s is bounded by and includes the following two sequences: GGCGCCGGCCGGACTGTGCAG (bases 1 to 21 of SEQ ID NO:2) and CCAGAGACTGCACCAGCGCAGCCC-AGCTTGAGCAAGATAGCG (SEQ ID NO:216, which is the result of joining bases 38144-38166 of SEQ ID NO:2 with bases 359-376 SEQ ID NO:2), and is defined by SEQ ID NO: 2.

Please replace the paragraph beginning at page 56, line 11 with the following amended paragraph:

In some of the samples of example 6 we typed a 4 bp deletion (dbSNP#3916791) located in the common portion of the sequences S1, S2 and S3 contiguous with sequence SEQ ID NO: 1. Specifically, the polymorphism is contained in the sequence GCGCCTGCCAAGAT*TGTC*TGAGTATTGATCGAACCC (bases 309-344 of SEQ ID NO:2), where the bases represented with boldface, italicised letters are present in some human chromosome 19 but not all. The deletion was typed by (1) Performing a PCR on the persons DNA with the primers 5'-6-FAM-TGAGACGAGGTGGAGG-3' (SEQ ID

NO:214) and 5'-CAATCAAAAAGAAAACATGG-3' (SEQ ID NO:215). The fluoroscein-containing (6-FAM) primer was obtained from TIB-MOLBIOL (Berlin, Germany), while the other primer was obtained from DNA-Technology (Aarhus, Denmark). The reaction mix contained 0.84 U Taq polymerase (Roche), 1.7 nmole of each dNTP, 5 pmole of each primer, 1X PCR buffer (Roche), 1 M betain and approximately 20 ng DNA in a total volume of 9 ul. We used a temperature program containing 4 min denaturation at 94 C, followed by 30 cycles of 96 C for 1 min, 55C for 30 sec, and 72 C for 45 sec; (2) We then mixed a sample containing 1 ul PCR product, 0.5 ul GeneScan-500 ROX size marker (Applied Biosystems) and 19 ul formamide; and (3) loaded the sample onto a single lane of Sequagel-6 matrix on a model 3100 Genetic Analyzer (ABI Prism, Applied Biosystems) using fluorescence detection. The persons who were homozygote for the complete fragment gave a length of 167 bp relative to the size markers, the persons who were homozygote for the 4 bp deletion gave a length of 163 bp, and the heterozygotes showed both lengths in roughly equimolar amounts. Because it has repeatedly been observed that the underlying risk-genotype seems recessive (Examples 2, 6, 7, 8), we pooled the homozygous low risk genotypes (163/163) and the heterogotes (163/167).